

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 18, 2003, 20:06:37 ; Search time 21 Seconds

(without alignments)
1159.362 Million cell updates/sec

Title: US-09-815-923-4

Sequence: 1 MPPSDAPPAPAPPPDLPAT.....TIOREVTSTPPADSLCNL 587

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2333.5	74.3	622	1	S6A4_DROME
2	1726	55.0	630	1	S6A4_HUMAN
3	1723	54.9	630	1	S6A4_CAVPO
4	1717	54.7	630	1	S6A4_MACMU
5	1716	54.6	630	1	S6A4_MOUSE
6	1712	54.5	630	1	S6A4_RAT
7	1706	54.3	630	1	S6A4_BOVIN
8	1629.5	51.9	617	1	S6A2_MOUSE
9	1608.5	51.2	615	1	S6A2_BOVIN
10	1605.5	51.1	617	1	S6A2_HUMAN
11	1558	49.6	693	1	S6A3_BOVIN
12	1542	49.1	620	1	S6A3_HUMAN
13	1539	49.0	619	1	S6A3_RAT
14	1538	49.0	619	1	S6A3_MOUSE
15	1412	45.0	615	1	NTDO_CAEEL
16	1368.5	43.6	797	1	S6A5_HUMAN
17	1363.5	43.4	799	1	S6A5_RAT
18	1358.5	43.3	599	1	S6A1_HUMAN
19	1347.5	42.9	598	1	S6A1_RAT
20	1329	42.3	598	1	S6A1_MUSCO
21	1309	41.7	598	1	S6A1_MOUSE
22	1298	41.3	635	1	S6A8_BOVIN
23	1286.5	41.0	635	1	S6A8_HUMAN
24	1282	40.8	635	1	S6A8_RAT
25	1279	40.7	635	1	S6A8_BOVIN
26	1279	40.7	635	1	S6A8_RABIT
27	1271	40.5	627	1	S6AB_MOUSE
28	1267	40.4	620	1	S6AB_MOUSE
29	1267	40.3	620	1	S6AC_CANFA
30	1256.5	40.0	614	1	S6AC_CANFA
31	1254	39.9	602	1	S6AD_RAT
32	1253.5	39.9	632	1	S6AB_HUMAN
33	1252	39.9	602	1	S6AD_MOUSE

34	1251.5	39.8	614	1	S6AC_RAT	P48056 rattus norv
35	1251	39.8	620	1	S6A6_HUMAN	P31641 homo sapien
36	1247.5	39.7	614	1	S6AC_HUMAN	P48065 homo sapien
37	1244.5	39.6	614	1	S6AC_RABIT	P48055 oryctolagus
38	1243	39.6	614	1	S6AC_MOUSE	P31651 mus musculu
39	1243	39.6	621	1	S6A6_RAT	P31643 rattus norv
40	1241	39.5	621	1	S6A6_MUSCO	P31642 mus cookil
41	1238.5	39.4	637	1	S6A7_RAT	P28573 rattus norv
42	1232.5	39.2	636	1	S6A7_HUMAN	O99884 homo sapien
43	1229	39.1	638	1	S6A9_BOVIN	O28039 bos taurus
44	1221	38.9	621	1	S6A6_MOUSE	O35316 mus musculu
45	1212	38.6	633	1	S6A9_RAT	P28572 rattus norv

ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	622 AA
AC	S6A4_DROME	09W1177:			
DT	01-OCT-1996 (rel. 34, Created)				
DT	01-OCT-1996 (rel. 34, Last sequence update)				
DT	16-OCT-2001 (rel. 40, Last annotation update)				
DE	Sodium-dependent serotonin transporter (5HT transporter) (5HTT)				
DE	(Cocaine-sensitive serotonin transporter).				
GN	SERT OR CGA545.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;				
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;				
OX	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_Taxid=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRATIN-Canton S; TISSUE=Head;				
RX	MEDLINE=94255490; PubMed=8197200;				
RA	Demchynshyn L.L., Pristupa Z.B., Sugamori K.S., Barker E.L.,				
RA	Blakely R.D., Wolfgang W.J., Forte M.A., Niznik H.B.;				
RT	*Cloning, expression, and localization of a chloride-facilitated,				
RT	cocaine-sensitive serotonin transporter from Drosophila				
RT	melanogaster.;				
RT	Proc. Natl. Acad. Sci. U.S.A. 91:5158-5162(1994).				
RT	[2]				
RC	SEQUENCE FROM N.A.				
RX	MEDLINE=20196006; PubMed=10731132;				
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,				
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,				
RA	Abrial J.F., Agbayani A., An H.-J., Andrews-Plankkoc C., Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhendari D., Bolshakov S.,				
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,				
RA	Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,				
RA	Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,				
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,				
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,				
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,				
RA	Merklov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,				
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,				
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,				
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,				

RA Relnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
 "The genome sequence of *Drosophila melanogaster*.";
 Science 287:2185-2195(2000).
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH
 CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
 CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
 CC FAMILY (SNF).

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CC EMBL: U04809; AAA19430.1; -
 CC EMBL: AE003464; AAF47200.1; -
 DR FlyBase: FBgn0010414; Sert.
 DR InterPro: IPR000175; Na/nttra-symport.
 DR Pfam: PF00209; SNF.1.
 DR PRINTS: PR00176; NANEUSMPORT.
 DR PRODOM: PD000448; Na/nttra-symport.1.
 DR PROSITE: PS00610; NA_NEUROTRAN_SYM_1; 1.
 DR PROSITE: PS00754; NA_NEUROTRAN_SYM_2; 1.
 DR PROSITE: PS50267; NA_NEUROTRAN_SYM_3; 1.
 KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
 KW Symport.
 FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 1 (POTENTIAL).
 FT TRANSMEM 111 130 2 (POTENTIAL).
 FT TRANSMEM 155 175 3 (POTENTIAL).
 FT DOMAIN 176 244 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 245 263 4 (POTENTIAL).
 FT TRANSMEM 272 289 5 (POTENTIAL).
 FT TRANSMEM 325 342 6 (POTENTIAL).
 FT TRANSMEM 354 375 7 (POTENTIAL).
 FT TRANSMEM 408 427 8 (POTENTIAL).
 FT TRANSMEM 455 473 9 (POTENTIAL).
 FT TRANSMEM 489 509 10 (POTENTIAL).
 FT TRANSMEM 530 549 11 (POTENTIAL).
 FT TRANSMEM 568 586 12 (POTENTIAL).
 FT DOMAIN 587 622 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 622 AA; 69325 MW; 8E100BA905A98D CRC64;

Query March 74.3% Score 2333.5; DB 1; Length 622;
 Best Local Similarity 76.5% Pred. No. 1.1e-145;
 Matches 434; Conservative 50; Mismatches 76; Indels 7; Gaps 4;

OY 8 PAPTAPPDLPATTAQKRSVVSLLTPARQRETWAKKAFFLLAVVGFVADLGNVWRPPI 67
 Db 47 PAKYTD--LAPKANNERRILVSVT--ERRRETGQGAFFLLAVVGFVADLGNVWRPPI 103
 OY 68 CYONGGCAFLIPYVLMFLGGCLPLFLELALGOYHRCGCLTLMKRICPALKGVAYICMI 127
 Db 104 CYONGGCAFLIPYVLMFLGGCLPLFLELALGOYHRCGCLTLMKRICPALKGVAYICMI 163
 OY 128 DIYGMVYNTTIGAVVYLLASINSVLPWTSQDMENPPLCTPTTSPTQNNSSTPA 187
 Db 164 DIYGMVYNTTIGAVVYLL--FASTSKLPWISCDNPMWNTNEMQVTSNFTELATSPA 220

OY 188 KEFFERLEQHKNGLDMDPIKPSLALCYGVGVLYFFSLMKGVRSAGKVVWVTAAP 247
 Db 221 KEFFERKLVESYKNGDPMKPVKPTLALCYGVGVLYFFSLMKGVRSAGKVVWVTAAP 280
 OY 248 YVLLILLARGLVLPGATEGIRYLLTPWHLKNSKWIDAASQIFSLGPGFTLLALS 307
 Db 281 YVLLILLARGLVLPGATEGIRYLLTPWHLKNSKWIDAASQIFSLGPGFTLLALS 340
 OY 308 SYNNFNNNCYDALITSSINCLTSFLAGFVFEVSLGMAHONKNSIEVEGEGGLVPIV 367
 Db 341 SYNNFNNNCYDALITSSINCLTSFLAGFVFEVSLGMAHONKNSIEVEGEGGLVPIV 400
 OY 368 YPEAIATMGSGVFVAIFLFLILILGLDSTFGGLEAVTALCDYPRVILGHRFEVAVL 427
 Db 401 YPEAIATMGSGVFVAIFLFLILILGLDSTFGGLEAVTALCDYPRVILGHRFEVAVL 460
 OY 428 LLEFYICALPTTYGGVLYVDLNVYGGALILFVFAEAGVQWGVDRFSDVPTML 487
 Db 461 LAFIFLCLPMTYGGVLYVDLNVYGGALILFVFAEAGVQWGVDRFSDVPTML 520
 OY 488 GHTPGMFRQWYSIIPVFLILFVFSYLAHEMLGGEYTPSPSITVGMWGTQVSCI 547
 Db 521 GSKPGLFMRICWTYISPVFLILFVFSYLAHEMLGGEYTPSPSITVGMWGTQVSCI 580
 OY 548 PLVITYKLLI--TPGNCINRIKTIOPE 573
 Db 581 PMVITYKFFFSKSGCRQRLQESFOPE 607

RESULT 2

S6A4_HUMAN STANDARD; PRT; 630 AA.

AC P31645;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Sodium-dependent serotonin transporter (5HT transporter) (5HTT).

GN SLC6A4 OR HTR OR SERT.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=93199744; PubMed=8452685;

RA Lesch K.P., Wolozin B.L., Estler H.C., Murphy D.L., Riederer P.;

"Isolation of a cDNA encoding the human brain serotonin transporter.";

RL J. Neural Transm. 91:67-73(1993).

RN (12)

RP SEQUENCE FROM N.A.

RX MEDLINE=93211998; PubMed=7681602;

RA Ramamoorthy S., Bauman A.L., Moore K.R., Han H., Yang-Feng T.,

Chang A.S., Ganapathy V., Blakely R.D.;

"Antidepressant- and cocaine-sensitive human serotonin transporter:"

molecular cloning, expression, and chromosomal localization.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:2542-2546(1993).

RN (13)

RP SEQUENCE FROM N.A.

RX MEDLINE=93260476; PubMed=7684072;

RA Lesch K.P., Wolozin B.L., Murphy D.L., Riederer P.;

"Primary structure of the human platelet serotonin uptake site:"

identity with the brain serotonin transporter.";

RL J. Neurochem. 60:2319-2322(1993).

RN (14)

RP SEQUENCE OF 1-114 FROM N.A.

RX TISSUE=Platelet;

RA Bradley C.C., Blakely R.D.;

Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 -1- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH
 AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.

```

CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SUBCELLULAR LOCATION: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
CC      STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
CC      -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC      FAMILY (SNP).
CC      -----
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CC      -----
DR      EMBL; X70697; CAAS0029.1; -
DR      EMBL; L05368; AAA35492.1; -
DR      EMBL; U79746; AAB93475.1; -
DR      PIR; S37688; S37688.
DR      PIR; A47398; A47398.
DR      GeneW; HGNC:11050; SLC6A4.
DR      MIM; 182138; -.
DR      InterPro; IPR002437; 5HT_transporter.
DR      InterPro; IPR000175; Na/ntran_symport.
DR      Pfam; PF00209; SNF_1.
DR      Pfam; PF03491; 5HT_transporter_1.
DR      PRINTS; PR00176; NANEUSMPORT.
DR      ProDom; PD000448; Na/ntran_symport; 1.
DR      PROSITE; PS00610; NA_NEUOTRAN_SYM_1; 1.
DR      PROSITE; PS00754; NA_NEUOTRAN_SYM_2; 1.
DR      PROSITE; PS50267; NA_NEUOTRAN_SYM_3; 1.
KW      Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW      Symport.
FT      DOMAIN            1      87      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM          88     108     1 (POTENTIAL).
FT      TRANSMEM         116     135     2 (POTENTIAL).
FT      TRANSMEM         160     180     3 (POTENTIAL).
FT      DOMAIN           181     252     EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM         253     271     4 (POTENTIAL).
FT      TRANSMEM         280     297     5 (POTENTIAL).
FT      TRANSMEM         333     350     6 (POTENTIAL).
FT      TRANSMEM         362     383     7 (POTENTIAL).
FT      TRANSMEM         417     436     8 (POTENTIAL).
FT      TRANSMEM         464     482     9 (POTENTIAL).
FT      TRANSMEM         498     518     10 (POTENTIAL).
FT      TRANSMEM         539     558     11 (POTENTIAL).
FT      TRANSMEM         577     595     12 (POTENTIAL).
FT      DOMAIN           630     630     CYTOPLASMIC (POTENTIAL).
FT      DOHAIND          596     630     N-LINKED (GLCNAC...) (POTENTIAL).
FT      CARBOHYD          217     217     N-LINKED (GLCNAC...) (POTENTIAL).
FT      SEQUENCE        630 AA; 70324 MW; 0EB535B0A579BDAA2 CRC64;
Query Match          55.0%; Score 1726; DB 1; Length 630;
Best Local Similarity 54.5%; Pred. No. 6-2e-106;
Matches 320; Conservative 97; Mismatches 154; Indels 16; Gaps 6
Oy      6 AAPAPTPAPP---DLPAATTAQSRNSVSVLPAPARETFWAKKAPELLAVGFAVDLGAWY 62
    1-1-1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      49 AVSPGAGDDTRHSIPATP-----TTVAELHQGERETMGKKVDFLLSYIGAYVDLGAWY 103
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      63 REPPTCYONGGGAFLIPYCWMLEFGGLDFLEFLALGOYHRGGCLTMKRITCPALKGVGY 122
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      104 REPPTCYONGGGAFLIPTMAIFGIDPLEFMELALGOYHRNGCISIMKRIIDPIRGIGY 163
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      123 AICMDIDMGVYNTIIIMAVYYVLASLASINSVLPMTSCDENENVTPLCTPYTSPT-- 179
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      164 AICIAPFIASYNTIMMALTYLL----SFIDQLPMTCCKNSMWTGCNCTINFSEDNITW 220
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      180 NPNSSTPAKEEFERNVLEOHKSNGIDMGPIKPRLSCALCVGFYVLVYSLMKGVSACKV 239
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      221 TLHSTPSAEFEYTRIVLIQHRSKGHODIGISMQLALCIMLFIVIFYSIIMKGVATSKCV 280
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      240 VVVVALAPYVVLIIILAGVTLPGATBSIRIYLLPEMHKLMSKVWDIASITFFSLGPG 299
    ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Dh 281 VMVATATFPYIIILSVLRGATLPCGAKRQVFLYKLRPNMQKLEETGVMIDAAQIIFPSLCRG 340
Oy 300 FGTLLAASYNKFNPNNCYRDALITSSINCLTSFLAGFYISVGLGYMAHVONKSTIEEYGLE 359
Dh 341 FGVLLAFASYNKFNPNNCYQDVALVTSVONCMTSFVSGFIEFVPLVGLVMAERREDYSEVAKD 400
Oy 360 -GPGVLVIVYEALATMTGSAFMAIIFPLMLITIGLDBSTFGCLGAVTALCDEYPRVLGR 418
Dh 401 AGPSLLEFVTAEEALANMPASTFEFAIIFPLMLITIGLDBSTFGALGCVITAVLDEDPHWAK 460
Oy 419 HREVFVAALVLFYICALPTTGGVYLVLDLNVYGPGLALIFVFAFAAGVCWVGVD 478
Dh 461 RREFVFLAVVITTCFPGSLVITLITFGCAIYVYKLEEAIGAPAVLITALLPAVAVSNFYGITQ 520
Oy 479 FSEDVFTMLGHTPGMFWRTCMYSIYSPVLLVLFVFSVLAHEMLEMGEETYPSSITVGWV 538
Dh 521 FCRDVKEMIGSPGMFMRICWVAISPLFLFICSFMSPPQLRFLRYNYPWYSIILGYC. 580
Oy 539 MTGTTVSGIPLIYIKLLITGNCINR-IKTIQREPVTSIPPADSTL 584
Dh 581 IGTSSFFICIPYIAYRLITITGTEKERIKMSITPETPEIPCQDIRL 627

RESULT 3
S6A4_CAVPO
ID S6A4_CAVPO STANDARD: PRT: 630 AA.
AC 035899;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium-dependent serotonin transporter (5HT transporter) (5HTT).
GN SLC6A4.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestinal mucosa;
RX MEDLINE=96180949; PubMed=8601815;
RA Wade P.R., Chen J., Jaffe B., Kassam I.S., Blakely R.D., Gershon M.D.;
RT "Localization and function of a 5-HT transporter in crypt epithelia
of the gastrointestinal tract."
RL J. Neurosci. 16:2352-2364(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestinal mucosa;
RA Chen J., Wade P.R., Rothman T.P., Gershon M.D.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH
AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
CC -I- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
FAMILY (SNEF).
CC -----
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CC -----
DR EMBL, U84498; AAB82737.1; -
DR InterPro: IPR002437; 5HT_transporter.
DR InterPro: IPR000175; Na/nttran_symport.
DR Pfam: PF00209; SNEF. 1.
DR Pfam: PF03491; 5HT_transporter; 1.
DR PRINTS: PR00176; NANEUSMPORT.
DR ProDom: PD000448; Na/nttran_symport; 1.
DR ProSite: PS00610; NA_NEUOTRAN_SYMPT_1; 1.

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OY 63 RPPYICYONGGAGFLIPYCMVLLFGSLDPLFLELALGQYHRCGCTLTKRICPALKGQY 122
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 104 RPPYICYONGGAGFLIPYCMVLLFGSLDPLFLELALGQYHRCGCTLTKRICPALKGQY 163
OY 123 AICMIDIYMGWYNTTIGMAYYYLLASINSVLPMTSCDNEWTPLCTPYTSQOT--- 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 164 AICIAFYASYNTIMAMALYYLL---SSFTDLPMTSCKSNMTGCTNFESDNTJTW 220
OY 180 NPNSTPAKFEFFERVLFOHKSNGIDMDGPIKSPALCVFGVLYVYSIMKGVASAGV 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 221 TLHSTSPAEFFTRVLDIHSKLGDDGGISWQALCLMLFTVYFSIMKGVATSGKV 280
OY 240 VVWATALAPYVLLILLARGVLLPGATEGIRYLYPEPMHKLONSKYWDIAASQIFPSLGG 299
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 261 VVWATPFYIILSVLLVGGATLPGAMRGVLFYFLKNMCKLLETGVMIDAAQIFPSLGG 340
OY 300 FGTLLALSINKFNKNCYRDALITSINCLNSFLAGFYFSVLYGMAYHONKSIEVGLE 359
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 341 FGVLAFASYNKFNKNCYQDALVTSVNCMTSFGVFIETVLGYMAERKNEDESEVAKD 400
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 360 -GPGVLFVYVPEAIVMTGVSVMATIFFLMLITLGLDSTFGGLEAVTALGDEYRVLGR 418
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 401 AGPSLFTFYAIAINMPASTFFALITFLMLITLGLDSTFAGLEGVITRAVLDEPHIMAK 460
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 419 HREVFVAVLLFTYICALPTTYGGVYLVLDLVNYPGLAILFVFAEAGVCMWYGVDR 478
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 461 RREMFVLAIVITCFEGLVTLFGGAYVYKLEEVATGPAVLTLAEVANASWRYGITO 520
OY 479 FSEDYRMLGHTPGFMRFCMSYISPVLELVFVSVAHEMLGGEYTPSWSTTVGMV 538
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 521 FCRDVKEMLGSPGFMFMRICVWAISPLFLFLICISFLSPOLRFOYNYPHMSITLGYC 580
OY 539 MTGTVSCIPLYIYIKLLITTPGNCINR-IKTQREPVTSIPADSTL 584
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 581 IGTSSFVCIPTIYIARLITRGTETREKRIKSTITPPEITPCGVRL 627

RESULT 5
S644_MOUSE
ID S644_MOUSE STANDARD: PRT: 630 AA.
AC 060857: 035241:
DT 15-JUL-1998 (rel. 36, created)
DT 15-JUL-1998 (rel. 36, last sequence update)
DT 16-OCT-2001 (rel. 40, last annotation update)
DE Sodium-dependent serotonin transporter (5HT transporter) (5HTT).
GN SLC6A4 OR 5HTT OR SERT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97189261; PubMed=9037532;
RA Chang A.S., Chang S.M., Starnes D.M., Schroeter S., Bauman A.L.,
RT Blakely R.D.;
RL "Cloning and expression of the mouse serotonin transporter.";
RN Brain Res. Mol. Brain Res. 43:185-192(1996).
RP [2]
RX SEQUENCE FROM N.A.
RC STRAIN=129;
RA MEDLINE=97225900; PubMed=9073170;
RA Bengel D., Hells A., Petri S., Seemann M., Glatz K., Andrews A.,
RT Murphy D.L., Lesch K.P.;
RL "Gene structure and 5'-flanking regulatory region of the murine
serotonin transporter.";
RN Brain Res. Mol. Brain Res. 44:286-292(1997).
RP [3]
RX SEQUENCE OF 1-114 FROM N.A.
RC STRAIN=BAUB/c;
RA Saito N., Sakai N., Kobayashi S., Fujimoto M., Morikawa O.,
RT Ikegaki N.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]

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RP SEQUENCE OF 69-630 FROM N.A.
RX MEDLINE=93283858; PubMed=8507984;
RA Gregor P., Patel A., Shlmade S., Lin C.L., Rochelle J.M., Kitayama S.,
RT Seldin M.F., Uhl G.R.;
RL "Murine serotonin transporter: sequence and localization to
chromosome 11.";
Mamm. Genome 4:283-284(1993).
CC -1- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH
AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
FAMILY (SMT).
CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 195.
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CC -----
DR EMBL: AF013604; AAB67172.1; -
DR EMBL: Y08870; CAA70092.1; -
DR EMBL: Y08871; CAA70092.1; JOINED.
DR EMBL: Y08872; CAA70092.1; JOINED.
DR EMBL: Y08873; CAA70092.1; JOINED.
DR EMBL: Y08874; CAA70092.1; JOINED.
DR EMBL: Y08875; CAA70092.1; JOINED.
DR EMBL: Y08876; CAA70092.1; JOINED.
DR EMBL: Y08877; CAA70092.1; JOINED.
DR EMBL: Y08878; CAA70092.1; JOINED.
DR EMBL: Y08879; CAA70092.1; JOINED.
DR EMBL: Y08880; CAA70092.1; JOINED.
DR EMBL: U26452; AAA84750.1; -
DR EMBL: X66119; -; NOT ANNOTATED_CDS.
DR MGI: 96285; Slc6a4.
DR InterPro: IPR002437; 5HT_transporter.
DR InterPro: IPR000175; Na/nttran_symport.
DR Pfam: PF00209; SMT_1.
DR Pfam: PF03491; 5HT_transporter_1.
DR PRINTS: PR000176; NANUSMPORT.
DR PRODOM: PD000448; Na/nttran_symport_1.
DR PROSITE: PS00610; NA_NEUROTRAN_SYM_1; 1.
DR PROSITE: PS00754; NA_NEUROTRAN_SYM_2; 1.
DR PROSITE: PS0267; NA_NEUROTRAN_SYM_3; 1.
KW Neurotransmitter transporter; Transport; Transmembrane; Glycoprotein;
KW Symport.
FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 108 1 (POTENTIAL).
FT TRANSMEM 116 135 2 (POTENTIAL).
FT TRANSMEM 160 180 3 (POTENTIAL).
FT DOMAIN 181 252 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 253 271 4 (POTENTIAL).
FT TRANSMEM 280 297 5 (POTENTIAL).
FT TRANSMEM 333 350 6 (POTENTIAL).
FT TRANSMEM 362 383 7 (POTENTIAL).
FT TRANSMEM 417 436 8 (POTENTIAL).
FT TRANSMEM 464 482 9 (POTENTIAL).
FT TRANSMEM 498 518 10 (POTENTIAL).
FT TRANSMEM 539 558 11 (POTENTIAL).
FT TRANSMEM 577 595 12 (POTENTIAL).
FT DOMAIN 596 630 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 217 217 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 196 196 P -> Q (IN REF. 2).
FT CONFLICT 415 415 A -> R (IN REF. 2).
SQ SEQUENCE 630 AA; 70147 MW; F37EFIECI164FB30 CRC64;
Query Match 54.6%; Score 1716; DB 1; Length 630;

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Best Local Similarity 54.3%; Pred. No. 2.8e-105;
Matches 317; Conservative 100; Mismatches 151; Indels 16; Gaps 6;

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OY 6 APPAPTA---PPDLPATTAQKSRSVVSLTPAROREWMAKAEPLAVGEFANDLGVW 62
D 49 AVPTSGADEAPHSPTPAT---TTLVAEIHOGEREHWGKMKPFLSVIGYAADLGNIM 103
OY 63 RFPYICONGGAGFLIPCYVMLFPGGLPFLFELALQGHKCGCGLTKRICKIPALCKGY 122
D 104 RFPYICONGGAGFLIPPTTMAIFGIGIFLFWELALQGHKCGCGLTKRICKIPALCKGY 163
OY 123 AICMIDYMGWYNTTIGMAVYVLIASINSVLPMTSCDNEWNTPLCTPVSPT-- 179
D 164 AICIAFIASYVNTIIMALYLYLI---SFTDQLPMTSCKNMNTGCTNYFADNITW 220
OY 180 NPNSSTPAKEFFENVELOHKSNGLDPMKPSALCFCGVFVLYVLSLKGVSAGV 239
D 221 TLHSTSPAEFYLHRHVLIQHOSKGLQDGTISWOLALCIMLFIITYFSIKRGVTSKV 280
D 240 VAVTALAPYVLLILLAGVTLPGATEGIRYVLPPEMHLONSKWIMDAASOIFSLGPG 299
D 281 VAVTATPFYIYVLSVLVAGATLPGAMRGVYVYELKPNMOKLETGVWVAAQIIFSLGPG 340
OY 300 FGLTLLASSYKFNNNCYRDLITSSINCLTSLAGVIFSVLGMAHVONKSIIEVGL 359
D 341 FGVLLAFASYKFNNNCYQDALYTSVNCMTSEVSGVIFVTLGYMAEMRVEDVSEVAKD 400
OY 360 -GRLVLYVPEALATMGVFNALIFPLMLITGLDSTEGGLEAVTALCDEYRVLGR 418
D 401 AGPSLFTVYEAIAANMPASFFAIFLPLMLITGLDSTEGGLEAVTALCDEYRVLGR 460
OY 419 HREVFVAVLLFIYICALPTTGGVYVLDLINVGPALIFVFAEAGVCWYGVDR 478
D 461 RRENFVLIVITCLIGSLTLTSGGAVYVTLLEEARPAVLIALLAVVSMYGTQ 520
OY 479 FSEDFRMLGHTPGFMFTCSYISPVFLVLFVSLAHEMUGETYSMTSTGVW 538
D 521 FCSVPEKMLGSPGMFMRICVVAISPLFLFICSFILMSPPQLRFQYVPHWSIILGYC 580
OY 539 MTGTVSCIPLYIKLITPGNCINR-IKTQREVSISPPAD 581
D 581 IGTSSVICIPYIIRLITSTPGTLKERIKITSTPTPEIPFCGD 624

RESULT 6
S6A4_RAT STANDARD: PRT: 630 AA.
P31652; P23976;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
DE Sodium-dependent serotonin transporter (5HT transporter) (5HTT).
GN SLC6A4.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar;
RC MEDLINE=92111740; PubMed=1765155;
RA Mayser W., Betz H., Schloos P.;
RT "Isolation of cDNAs encoding a novel member of the neurotransmitter
RT transporter gene family.";
RL FEBS Lett. 295:203-206(1991).
RN 12
RP SEQUENCE FROM N.A.
RP TISSUE=Brain stem;
RC MEDLINE=92049754; PubMed=1944572;
RA Blakey R.D., Berson H.E., Fremieu R.T. Jr., Caron M.G., Peek M.M.,
RA Prince H.K., Bardley C.C.;
RT "Cloning and expression of a functional serotonin transporter from
RT rat brain.";

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RL Nature 354:66-70(1991).
RN [3]
RP REVISIONS.
RC TISSUE=Brain stem;
RA Blakey R.D.;
RN Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=92054541; PubMed=1948036;
RA Hoffman B.J., Mezey E., Brownstein M.J.;
RT "Cloning of a serotonin transporter affected by antidepressants.";
RT Science 254:579-580(1991).
RN 5
RP SEQUENCE FROM N.A.
RC STRAIN=Fawn hooded;
RA Gonzalez A.M., Smith A.P.L., Emery C.J., Higgenbottom T.W.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH
CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC FAMILY (SMF).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X63995; CAA45401.1; -
DR EMBL: X63253; CAA44913.1; -
DR EMBL: M79450; AAA42186.1; -
DR EMBL: Y11024; CAA71909.1; -
DR PIR: S30604; S30604.
DR PIR: S19585; S19585.
DR InterPro: IPR002437; 5HT transporter.
DR InterPro: IPR000175; Na/ntan_symport.
DR Pfam: PF00209; SMF; 1.
DR Pfam: PF03491; 5HT_transporter; 1.
DR PRINTS: PR00176; NANEUSMPORT.
DR ProDom: PD000448; Na/ntan_symport; 1.
DR PROSITE: PS00610; NA_NEUROTRAN_SYM_1; 1.
DR PROSITE: PS00754; NA_NEUROTRAN_SYM_2; 1.
DR PROSITE: PS00267; NA_NEUROTRAN_SYM_3; 1.
KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW Symport.
FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 108 1 (POTENTIAL).
FT TRANSMEM 116 135 2 (POTENTIAL).
FT TRANSMEM 160 180 3 (POTENTIAL).
FT DOMAIN 181 252 4 (POTENTIAL).
FT TRANSMEM 253 271 5 (POTENTIAL).
FT TRANSMEM 280 297 6 (POTENTIAL).
FT TRANSMEM 333 350 7 (POTENTIAL).
FT TRANSMEM 362 383 8 (POTENTIAL).
FT TRANSMEM 417 436 9 (POTENTIAL).
FT TRANSMEM 464 482 10 (POTENTIAL).
FT TRANSMEM 498 518 11 (POTENTIAL).
FT TRANSMEM 539 558 12 (POTENTIAL).
FT TRANSMEM 577 595 12 (POTENTIAL).
FT DOMAIN 596 630 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 415 415 A -> G (IN REF. 4).
FT CONFLICT 533 536 PGME -> GNV (IN REF. 4).
FT CONFLICT 621 630 PCGDIRMANV -> RVGHPHCCVTHPHRGHLFPATLSLSE
FT KPTGLL (IN REF. 4).
SQ SEQUENCE 630 AA: 70171 MW: 44DAVC5888C403EE CRC64;

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Db 401 AGPSLFTYEAANMPASTFEFAVFMILITLGLDSTFAGLEGVITAVLDEPHVMAK 460
QY 419 HREVEVAULLFETICALPTTYGGVYVLDLNVYGPGLATLFVFAEAGVCMVYDVR 478
Db 461 RREMFVGLGVITTCFFGSLVTLTGCAVYVKKLEEFATPPALVTALIAVAVEMVGINO 520
QY 479 FSEEDRTMLGHTPGFMFRTCMYSISPVLVLFVFSVLAHEMLGCEYTPSMTITGVV 538
Db 521 FCSVDKEMLGFSFGFMKICVVAISPLFLFICFSFLMSPQRLRFQDYDPRMSITLGYC 580
QY 539 MTGTTVSCIPLYIYIKLLITPNCINR-IKTIQREVSSTPADSTL 584
Db 581 IGTSFICIPYIYIRLVPTGLTKERIKGIPETPAIRPGDIRL 627

RESULT 8
S6A2_MOUSE STANDARD: PRT: 617 AA.
ID 56A2_MOUSE 05192:
AC 15-DEC-1998 (Rel. 37, Created)
AC 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium-dependent noradrenaline transporter (norepinephrine transporter) (NET).
GN SLC6A2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=98264327; PubMed=9603188;
RA Fritz J.D., Jayanthi L.D., Thoreson M.A., Blakely R.D.: "Cloning and chromosomal mapping of the murine norepinephrine transporter." 70:2241-2251(1998).
RL J. Neurochem. 70:2241-2251(1998).
CC -1- FUNCTION: TERMINATES THE ACTION OF NORADRENALINE BY ITS HIGH AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER FAMILY (SMF).
CC -----
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CC -----
DR EMBL: U76306; AAB94302.1; -
DR MGI: 1270850; Slc6a2.
DR InterPro: IPR001175; Na/ntra_nsymport.
DR Pfam: PF00209; SMF; 1.
DR PRINTS: PR00176; NANEUSMPORT.
DR PRODOM: PD000448; Na/ntra_nsymport; 1.
DR PROSITE: PS00610; NA_NEUTROTAN_SYM_1; 1.
DR PROSITE: PS00754; NA_NEUTROTAN_SYM_2; 1.
DR PROSITE: PS00754; NA_NEUTROTAN_SYM_3; 1.
KW Neurotransmitter transporter; Transport; Transmembrane; Glycoprotein; Symport.
FT DOMAIN 1 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 1 (POTENTIAL).
FT TRANSMEM 93 112 2 (POTENTIAL).
FT TRANSMEM 136 156 3 (POTENTIAL).
FT DOMAIN 157 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 253 4 (POTENTIAL).
FT TRANSMEM 262 279 5 (POTENTIAL).
FT TRANSMEM 315 332 6 (POTENTIAL).
FT TRANSMEM 344 365 7 (POTENTIAL).

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FT TRANSMEM 398 417 8 (POTENTIAL).
FT TRANSMEM 444 462 9 (POTENTIAL).
FT TRANSMEM 478 498 10 (POTENTIAL).
FT TRANSMEM 519 538 11 (POTENTIAL).
FT TRANSMEM 557 575 12 (POTENTIAL).
FT CAROHD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 617 AA: 69162 MW: AAB4412468BF59D CRC64;

Query Match
Best Local Similarity 51.9%; Score 1629.5; DB 1; Length 617;
Matches 310; Conservative 104; Mismatches 154; Indels 27; Gaps 9;

1 MPPSDAPPAPAP-----PDLPATTAQ-----KSRSVVSL-----TPARQETMAKKEF 47
Db 6 MNPQVQPELGADPLPEQPLRCKRADLLVYKERNVOCCLASQSDQAPRHWCKKIDF 65
QY 48 LLAVGFVAVDLGNVWRFPYICVONGGAFLLPYCYMLLEGLPLFLELALGQVHRCGL 107
Db 66 LLSVGFVAVDLGNVWRFPYICVONGGAFLLPYCYMLLEGLPLFLELALGQVHRCGL 125
QY 108 TLMKRICALGVGAICMIDLYMGMYNTIIGAAVYLLIASINSVLPMTSCDNEMN 167
Db 126 TWK-ICPFKGVGVAVILIALYVGFYVNIAMSLVYLFASF-TLN--LPWTNGHSMN 181
QY 168 TPLCT-----PVTSPOT--NPNSSTPAKEFFERNVLEQHSNGLDMDGPIKPSALCV 218
Db 182 SPNCIDPKLLNLSVGLDHTKYSKYFPAEYERGVGLHHESSGIDHIGLPQWLLIQL 241
QY 219 FGVEVLVYFSLMKGVRSAGKVVWATAPVYVLLILARGVTLPGATGIRVYLTPEWHK 278
Db 242 MVIIVLVYFSLMKGVRSAGKVVWATAPVYVLLILARGVTLPGATGIRVYLTPEWHK 301
QY 279 LONSVMVIDAASQIFSGPFGTLLASVKNENNCYRDALLSTINCLTSPLAGVY 338
Db 302 LKEATVWIDAAQIFSGAGGVGLIAPASTNKPENNCRDALLSTINCLTSPLAGVY 361
QY 339 FSVLYGMHVNOKSIEEVLGEGPGLVFIYVPEAIVTMTGSVFMAITFLMLITGLDSTF 398
Db 362 FSLIYGMHVNEDVATBEGAGVFLIYPAISTLSGSTFMAVLFMLALGLDSDM 421
QY 399 GGLVAVTALCDEYRVGRHREVVAVLLFETICALPTTYGGVYVLDLNVYGPGLA 458
Db 422 GGMVAVITGLADDF-QVLRHRKRLFTCVVITSTFLAFCITKGGIYVLTLDFTFAAGTS 480
QY 499 ILFVFAEAGVCMVYGVDRSEDRVTLGHTPGFMFRTCMYSISPVLVLFVFSVLAH 518
Db 481 ILFVFAEAGVCMVYGVDRSNDIQOMNGRPGIYKMLCKKFPVAPALLFVAVVSIINF 540
QY 519 EEMLGEEYTPSMTITGVWMTGTTVSCIPLYIYIKLLITPNCINRIKTQREPE 573
Db 541 KPLTDYDYTPPMANWVGMSIALSMILVPAVYIKFLIRGSLMERVAAYGITPE 595

RESULT 9
S6A2_BOVIN STANDARD: PRT: 615 AA.
ID 56A2_BOVIN P51143:
AC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium-dependent noradrenaline transporter (Norepinephrine transporter) (NET).
GN SLC6A2 OR NORADR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal medulla;
RX MEDLINE=94200377; PubMed=8150077;

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RA Lingen B., Bruns M., Boenisch H.;
 RT "Cloning and expression of the bovine sodium- and chloride-dependent
 RL noradrenaline transporter";
 RL FEBS Lett. 342:235-238(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE-Adrenal medulla;
 RX MEDLINE=95123332; PubMed=7823028;
 RA Jursky F., Tamura S., Tamura A., Mandiyan S., Nelson H., Nelson N.;
 RT "Structure, function and brain localization of neurotransmitter
 RL transporters";
 RL J. Exp. Biol. 196:283-295(1994).
 CC -1- FUNCTION: TERMINATES THE ACTION OF NORADRENALINE BY ITS HIGH
 CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SODIUM-NEUROTRANSMITTER SYMPORTER
 CC FAMILY (SNF).
 CC -----
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 CC -----
 CC EMBL: X79015; CA55645.1; -
 CC EMBL: U09198; AA82153.1; -
 CC InterPro: IPR00175; Na/ntra_n_symport.
 DR Pfam: PF00209; SNF; 1.
 DR PRINTS: PR00176; NANEUSMPORT.
 DR PRODOM: PD000448; Na/ntra_n_symport; 1.
 DR PROSITE: PS00610; NA_NEUROTRAN_SYM_1; 1.
 DR PROSITE: PS00754; NA_NEUROTRAN_SYM_2; 1.
 DR PROSITE: PS0267; NA_NEUROTRAN_SYM_3; 1.
 KW Neurotransmitter transporter; Transport; Transmembrane; Glycoprotein;
 KW Symport.
 FT DOMAIN 1 62 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 63 83 1 (POTENTIAL).
 FT TRANSMEM 91 110 2 (POTENTIAL).
 FT TRANSMEM 134 154 3 (POTENTIAL).
 FT DOMAIN 155 232 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 233 251 4 (POTENTIAL).
 FT TRANSMEM 260 277 5 (POTENTIAL).
 FT TRANSMEM 313 330 6 (POTENTIAL).
 FT TRANSMEM 342 363 7 (POTENTIAL).
 FT TRANSMEM 396 413 8 (POTENTIAL).
 FT TRANSMEM 442 460 9 (POTENTIAL).
 FT TRANSMEM 476 496 10 (POTENTIAL).
 FT TRANSMEM 517 536 11 (POTENTIAL).
 FT TRANSMEM 555 573 12 (POTENTIAL).
 FT DOMAIN 574 615 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 72 72 V -> L (IN REF. 2).
 FT CONFLICT 544 544 D -> V (IN REF. 2).
 FT CONFLICT 585 615 RLACTIPASEHHLVAORDIRFOLOHMLAI ->
 FT SEQUENCE 615 AA: 68899 MM: 828EF7691FDABFC6 CRC64;
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 Query Match 51.2%; Score 1608.5; DB 1; Length 615;
 Best Local Similarity 50.9%; Pred. No. 2.9e-98;
 Matches 296; Conservative 107; Mismatches 146; Indels 33; Gaps 7;

OY 121 GVAICMIDIMQMYNTIIGMAVYYLLASINSVLPFSCDNEMNPLCTPVTSPOTN 180
 DB 136 GCAVILIALYVCFYNNVIAHSLYYL-----FSSFTPLPMTDCGHMNSPNC-----TD 185
 OY 181 P-----NS-----TPAKEFFERNVLEQHSKSGLDMDGPIKPSLALCYGVEVL 224
 DB 186 PKLLNSVLYGNHTKYSKYKFTPAAEFYERGVHLHSSGIDHIGLPQMDLLITIVIV 245
 OY 225 VFFSLMKVRSAGKVVMTALAPYVLLILARGTGLGATGATGYTLPEHKKIONSKV 284
 DB 246 LFFSLMKGVKTSIGKVVMTALPVLVPLVGHITLPGASNGINAVLHIDIRKEATV 305
 OY 285 WIDASQIFESFGPGFTLLASYNKFNMCNCPALITSSNCLTSPFAGVFSVGY 344
 DB 306 WIDATQIFESFGAGFVLIAFASINKNDNCRALTLSTINCTSFISGATFSILGY 365
 OY 345 MAHVONKSTIEVGLGPGFLVPEALATMTGSVMAIIFPLMLITGLDSTFGLEAV 404
 DB 366 MAHEKVNIEDVATGAGLFLIYPEALSTIGSFMAIVFIMLALGIDSSMGMEAV 425
 OY 405 TTLADDEPRVLRREVFVAVLLFIYICALPTTYGCVLYVDLNNYGPALLPVF 464
 DB 426 ITGLADDF-QVLRHRKRLTFEAVSGFTPLALFCITKGIYVLTLDTFACSTILFVL 484
 OY 465 AEAAGVCWYGVDRSEDEVRTMLGHPGFWFRTCSYISPVLLVLFPSVLAHEMLGG 524
 DB 485 MEATVSNFYGVDRSNDIQOMGFRPGLYMLCKEYSPAPLLELVVLSITNRPITYD 544
 OY 525 EYTPSWSITVGMVMTGTTVSCIPLYIYKLLITPGNCINRI 566
 DB 545 DYIFPLMNMWGMGIAGSSMVLVPAYIVYKFFSTGSTRERL 586

RESULT 10
 S6A2_HUMAN
 ID S6A2_HUMAN STANDARD; PRT; 617 AA.
 AC P23975;
 DT 01-MAR-1992 (rel. 21, Created)
 DT 01-MAR-1992 (rel. 21, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Sodium-dependent noradrenaline transporter (Norepinephrine
 DE transporter) (NET).
 GN SLG6A2 OR NAT1 OR NET1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91179515; PubMed=2008212;
 RA Pacholczyk T., Blakely R.D., Amara S.G.;
 RT "Expression cloning of a cocaine- and antidepressant-sensitive human
 RL noradrenaline transporter";
 RL Nature 350:350-354(1991).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=96028030; PubMed=7488042;
 RA Poerzgen P., Boenisch H., Bruns M.;
 RT "Molecular cloning and organization of the coding region of the human
 RL norepinephrine transporter gene";
 RL Biochem. Biophys. Res. Commun. 215:1145-1150(1995).
 RN [3]
 RP VARIANT OI PRO-457.
 RX MEDLINE=20132303; PubMed=10684912;
 RA Shannon J.R., Plattem N.L., Jordan J., Jacob G., Black B.K.,
 RA Biaggioni I., Blakely R.D., Robertson D.;
 RT "Orthostatic intolerance and tachycardia associated with
 RL norepinephrine-transporter deficiency";
 RL New Engl. J. Med. 342:541-549(2000).
 CC -1- FUNCTION: TERMINATES THE ACTION OF NORADRENALINE BY ITS HIGH
 CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- DISEASE: DEFECTS IN SLC6A2 ARE A CAUSE OF ORTHOSTATIC INTOLERANCE
 CC (OI), A SYNDROME CHARACTERIZED BY LIGHTHEADEDNESS, FATIGUE,
 CC ALTERED MENTATION AND SYMPOE. IT IS ASSOCIATED WITH POSTURAL
 CC TACHYCARDIA. PLASMA NOREPINEPHRINE CONCENTRATION IS ABNORMALLY
 CC HIGH.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
 CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
 CC FAMILY (SNE).
 CC -----
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 CC -----
 CC EMBL; M65105; AAAS9943.1; -;
 CC EMBL; X91117; CA662566.1; JOINED.
 CC EMBL; X91120; CA662566.1; JOINED.
 CC EMBL; X91121; CA662566.1; JOINED.
 CC EMBL; X91122; CA662566.1; JOINED.
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 CC EMBL; X91125; CA662566.1; JOINED.
 CC EMBL; X91126; CA662566.1; JOINED.
 CC EMBL; X91127; CA662566.1; JOINED.
 CC EMBL; X91128; CA662566.1; JOINED.
 CC EMBL; X91119; CA662566.1; JOINED.
 CC PIR; S14278; S14278.
 CC GeneW; HGNC:11048; SLC6A2.
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 CC PROSITE; PS02067; NA_NEUROTRAN_SYM_3; 1.
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 KW Symport; Disease mutation; Polymorphism;
 FT DOMAIN 1 64 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 65 85 1 (POTENTIAL).
 FT TRANSMEM 93 112 2 (POTENTIAL).
 FT TRANSMEM 136 156 3 (POTENTIAL).
 FT DOMAIN 157 234 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 235 253 4 (POTENTIAL).
 FT TRANSMEM 262 279 5 (POTENTIAL).
 FT TRANSMEM 315 332 6 (POTENTIAL).
 FT TRANSMEM 344 365 7 (POTENTIAL).
 FT TRANSMEM 398 417 8 (POTENTIAL).
 FT TRANSMEM 444 462 9 (POTENTIAL).
 FT TRANSMEM 478 498 10 (POTENTIAL).
 FT TRANSMEM 519 538 11 (POTENTIAL).
 FT DOMAIN 557 575 12 (POTENTIAL).
 FT TRANSMEM 576 617 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 69 69 V -> I (IN DBSNP:1805064).
 FT VARIANT 99 99 T -> I (IN DBSNP:1805065).
 FT VARIANT 245 245 V -> I (IN DBSNP:1805066).
 FT VARIANT 292 292 N -> T (IN DBSNP:5563).
 FT VARIANT 356 356 V -> L (IN DBSNP:5565).
 FT VARIANT 369 369 A -> P (IN DBSNP:5566).
 FT /FTID=VAR_011761.

FT VARIANT 375 375 N -> S (IN DBSNP:5567).
 FT /FTID=VAR_011762.
 FT VARIANT 457 457 A -> P (IN OI: LOSS OF FUNCTION).
 FT /FTID=VAR_010022.
 FT VARIANT 463 463 K -> R (IN DBSNP:5570).
 FT /FTID=VAR_011763.
 FT VARIANT 478 478 G -> S (IN DBSNP:1805067).
 FT /FTID=VAR_011764.
 FT VARIANT 528 528 F -> C (IN DBSNP:5558).
 FT /FTID=VAR_011765.
 FT VARIANT 548 548 Y -> H (IN DBSNP:5559).
 FT /FTID=VAR_011766.
 SQ SEQUENCE 617 AA: 69332 MW: BDC6DF31316907BB CRC64;
 Query Match 51.1%; Score 1605.5; DB 1; Length 617;
 Best local similarity 51.6%; Pred. No. 4.6e-98;
 Matches 307; Conservative 106; Mismatches 155; Indels 27; Gaps 10;
 QY 1 MPPSDAPP---APPAAPPDLPA-TTAQ---KSRSVVSLT---PARORETAKKAEE 47
 DB 6 MNPQVQPENNNGADTGEQPLARKRTAELLVYKERNVGCLLAPRDGAQPRETWGKKIDF 65
 QY 48 LLAYGFAVDLGNVRFYICYNQNGAFILPYCMLPLFGGLPLFLELAGQYHRCCL 107
 DB 66 LLSVGFVAVDLANWRFPLCYCKNGGAFILPYLFLFIACMPLEFYMELALGOYNREGAA 125
 QY 108 TLMKRICPALKGVGGAICMIDIYMGMYNTIIGNAVYLLIASLSINSVLPMWPCSDNEMN 167
 DB 126 TWMK-ICPFPGKGVAVLLIALYGFYVNIAMSLLYLFSSF-TLN--LMTDCGHWN 181
 QY 168 TPLECT-----PVTSPT--NPNSSTPAKEFFERNVLEQHSNGLDMDGPIKPSLALCV 218
 DB 182 SPNCTDPKLLNGSVLGNHTKYSKYKFTPAEFYERGVHLHSSGIDHIGLPQMOLLCL 241
 QY 219 FGVFLVYFSLMKGYRSKGVYVWATAPYVLLILLARGTLPATGIRYVLPREHK 278
 DB 242 MYYVIVLVFSLMKGVKTSKGKVVMTATLPYLVFLVHGVTLPRASNGINAVLHIDFYR 301
 QY 279 LQNSKVMIDAASQIEFSLGPGFTLLALSYNKFNNNCYRALITSSINCLTSPFLAGFVI 338
 DB 302 LKEATVWIDANTQIFFSLAGPGVLIAPASVKNKPNKRRALLTSSINCITSPFSFGAI 361
 QY 339 FSVLGYMAHVONKSTIEVGLGPGGLVTPYEDATATMGSPWALIFPLMLITGLDSTF 398
 DB 362 FSLILGYMAHEKRVNIEDVATGAGLVFLYPEALISTLSTGTFMAVVFVMLALGLDSSM 421
 QY 399 GLEAVETALDDEYPRVGRHREYVAVLLFIYCALPTTYGGVYVLDLLVNYGELA 458
 DB 422 GGMFAVITGLADDF-QVLRHRKLETFGVTSTFLALFCITKGIVYLLDLPFAAGTS 480
 QY 459 ILFVFAEAGVCWYGVDRSEEDVRTMLGHTPGMFNRTCMYSIPVELLVFVSVAH 518
 DB 481 ILFVLMALIGVSMGYGDRSNDIQMMGFRPGIYMWLCKRFPSPALLLVVYVSIIN 540
 QY 519 EBMIGCEYTVSWSITFGWMTGTTVSCIPLYIKLLITPGNCINRIKTIQORPE 573
 DB 541 KPLTVDYIFPPMANWVGIALSSMLVPIYVLYKFLSTGSLMERLAVGITPE 595
 RESULT 11
 SGA3_BOVIN
 AC SGA3_BOVIN STANDARD: PRT: 693 AA.
 ID P27922;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sodium-dependent dopamine transporter (DA transporter) (DAT).
 GN SLC6A3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain:
RX MEDLINE=92107910; PubMed=1722321;
RA Usdin T.B., Mezey E., Chen C., Brownstein M.J., Hoffman B.J.;
RT "Cloning of the cocaine-sensitive bovine dopamine transporter.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:11168-11171(1991).
CC -1- FUNCTION: TERMINATES THE ACTION OF DOPAMINE BY ITS HIGH
    AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
    STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
    FAMILY (SNF).
CC -----
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    or send an email to license@isb.slb.ch).
CC -----
CC EMBL: M80234; -; NOT_ANNOTATED_CDS.
CC PIR: A41617; A41617.
CC InterPro: IPR000175; Na/nttran_symport.
CC DR InterPro: IPR001230; Prenyl_site.
CC DR Pfam: PF00209; SNF_1.
CC DR PRINTS: PR00176; NANEUSMPORT.
CC DR PRODOM: PD000448; Na/nttran_symport; 1.
CC DR PROSITE: PS00610; NA_NEUROTRAN_SYM_1; 1.
CC DR PROSITE: PS00754; NA_NEUROTRAN_SYM_2; 1.
CC DR PROSITE: PS0267; NA_NEUROTRAN_SYM_3; 1.
CC KM Neurotransmitter transport; Transmembrane; Glycoprotein;
    Symport.
CC FT DOMAIN 1 68
    FT TRANSMEM 69 89 CYTOPLASMIC (POTENTIAL).
    FT TRANSMEM 97 116 1 (POTENTIAL).
    FT TRANSMEM 140 160 2 (POTENTIAL).
    FT DOMAIN 161 234 3 (POTENTIAL).
    FT TRANSMEM 235 253 EXTRACELLULAR (POTENTIAL).
    FT TRANSMEM 262 279 4 (POTENTIAL).
    FT TRANSMEM 315 332 5 (POTENTIAL).
    FT TRANSMEM 344 365 6 (POTENTIAL).
    FT TRANSMEM 398 417 7 (POTENTIAL).
    FT TRANSMEM 444 462 8 (POTENTIAL).
    FT TRANSMEM 478 498 9 (POTENTIAL).
    FT TRANSMEM 519 538 10 (POTENTIAL).
    FT TRANSMEM 557 575 11 (POTENTIAL).
    FT TRANSMEM 576 693 CYTOPLASMIC (POTENTIAL).
    FT DOMAIN 181 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
    FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
    FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
    FT SEQUENCE 693 AA; 75691 MW; 0023A6F6D0698660 CRC64;

Query Match 49.6%; Score 1558; DB 1; Length 693;
Best local Similarity 50.1%; Pred. No. 6,7e-95;
Matches 283; Conservative 106; Mismatches 152; Indels 24; Gaps 6;

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Db 212 EFERGVLLHESOGIDDLGPPRMQLTSLVLVILLYFLSLMGVKTSGKVVITATMPY 271
QY 249 VVLIILLARCVTLPGATEGIRYTLTPEMHKLQNSKWIDAASQIFSLGCGFTLALSS 308
Db 272 VVLFALLRLGRTLPGAADAIKRAVLSDVFNRLCASAVIDAIAICFSLGGLVLAFFSS 331
QY 309 YNFENNNCYDALITSSINCLTSLGGLVYFVSUAGVAHQNSIEVEGLEGGLVITY 368
Db 332 YNFETNCRIDALITTSVNSLTSSFGVYFSELGLYMAQKHSVPICGVAKDQGLITTY 391
QY 369 PEAIATMTGSFMAIIFFLMLITLGLDSTFGLEAVTALCDEYPRVLRHREFAVLL 428
Db 392 PEALATLPSSWAVVEFVWLLTLTGIDISAMGMSVITGLADE-QLHRRHREFTLVV 450
QY 429 LFTYICALPTTGGVYLVLDLNVYGGALILEVFAEAGVCWYGVDFSEDVFTMLG 488
Db 451 LAFELLFLFCVTGNGIVYVFLDLHFAGTSTLEGVLMVEYGVWFMFGVQFSDIKQMTG 510
QY 489 HTFGWFRTGWSYISPFELLVLFVSVLAHEEMLGERTYPSMSITGVWMTGTSCIP 548
Db 511 RRSVLWRCLWKVYVSPCFLLFVYVVSATIRPPHYGAYVPEPNATLALMAAASSNVP 570
QY 549 LVYIYKLLTPPGNCINRIKTIORPE 573
Db 571 IYAAVKLCSLPGSSREKLAIVATPE 595

RESULT 12
56A3_HUMAN STANDARD; PRT; 620 AA.
ID 56A3_HUMAN STANDARD; PRT; 620 AA.
AC Q01959; Q14966;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium-dependent dopamine transporter (DA transporter) (DAT).
GN SLC6A3 OR DAT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93061810; PubMed=1359373;
RA Vandenbergh D.J., Persico A.M., Uhl G.R.;
RT "A human dopamine transporter cDNA predicts reduced glycosylation,
    displays a novel repetitive element and provides racially-dimorphic
    tagi RFLPs.";
RL Brain Res. Mol. Brain Res. 15:161-166(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93024326; PubMed=1406597;
RA Giorgi B., el Mestikawy S., Godinot N., Zheng K., Han H.,
    Yang-Feng T., Caron M.G.;
RT "Cloning, pharmacological characterization, and chromosome assignment
    of the human dopamine transporter.";
RL Mol. Pharmacol. 42:383-390(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=94134051; PubMed=8302271;
RA Pristupa Z.B., Wilson J.M., Hoffman B.J., Kish S.J., Niznik H.B.;
RT "Pharmacological heterogeneity of the cloned and native human
    dopamine transporter: dissociation of [3H]WIN 35,428 and [3H]GBR
    12,935 binding.";
RL Mol. Pharmacol. 45:125-135(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97444282; PubMed=9300814;
RA Kawarai T., Kawakami H., Yamamura Y., Nakamura S.;
RT "Structure and organization of the gene encoding human dopamine
    transporter.";
RL Gene 195:11-18(1997).

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[5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-20349832; PubMed-10889531;
 RA Vandenbergh D.J., Thompson M.D., Cook E.H., Bendahou E., Nguyen T.,
 RA Krasowski M.D., Zarblan D., Comings D., Sellers E.M., Tyndale R.F.,
 RA George S.R., O'Dowd B.F., Uhl G.R.;
 RT "Human dopamine transporter gene: coding region conservation among
 RT normal, Tourette's disorder, alcohol dependence and attention-deficit
 RT hyperactivity disorder populations."; Mol. Psych. 5:283-292(2000).
 RL [6]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-21200925; PubMed-11304827;
 RA Greenwood T.A., Alexander M., Keck P.E., McElroy S., Sadovnick A.D.,
 RA Remick R.A., Kelsoe J.R.;
 RT "Evidence for linkage disequilibrium between the dopamine transporter
 RT and bipolar disorder."; Am. J. Med. Genet. 105:145-151(2001).
 RL [7]
 RN SEQUENCE OF 1-385 FROM N.A.
 RX MEDLINE-95364623; PubMed-7637582;
 RA Donovan D.M., Vandenbergh D.J., Perry M.P., Bird G.S., Ingersoll R.,
 RA Nanchakumar E., Uhl G.R.;
 RT "Human and mouse dopamine transporter genes: conservation of
 RT 5'-flanking sequence elements and gene structures."; Brain Res. Mol. Brain Res. 30:327-335(1995).
 RL [8]
 RN SEQUENCE OF 164-255 FROM N.A.
 RX MEDLINE-92357778; PubMed-1353885;
 RA Bannion M.J., Poosch M.S., Xia Y., Goebel D.J., Cassin B.,
 RA Kapatos G.;
 RT "Dopamine transporter mRNA content in human substantia nigra
 RT decreases precipitously with age."; Proc. Natl. Acad. Sci. U.S.A. 89:7095-7099(1992).
 RL [9]
 RN FUNCTION: TERMINATES THE ACTION OF DOPAMINE BY ITS HIGH
 RT AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
 RL [10]
 RN SUBCELLULAR LOCATION: Integral membrane protein.
 RL [11]
 RN MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
 RT STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
 RL [12]
 RN SIMILARITY: BELONGS TO THE SODIUM-NEUROTRANSMITTER SYMPORTER
 RT FAMILY (SNP).
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 CC -----

DR EMBL: D88564; BAA22511.1; JOINED.
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 DR EMBL: D88566; BAA22511.1; JOINED.
 DR EMBL: D88567; BAA22511.1; JOINED.
 DR EMBL: D88568; BAA22511.1; JOINED.
 DR EMBL: D88569; BAA22511.1; JOINED.
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 DR GeneW: HGNC:11049; SLC6A3.
 DR MIM: 126455; -
 DR InterPro: IPR000175; Na/nttran_symport.
 DR Pfam: PF00209; SNE_1.
 DR PRINTS: PRO0176; NANEUSMPORT.
 DR ProDom: PD000448; Na/nttran_symport; 1.
 DR PROSITE: PS00610; NA_NEUROTRAN_SYM_1; 1.
 DR PROSITE: PS00754; NA_NEUROTRAN_SYM_2; 1.
 DR PROSITE: PS0267; NA_NEUROTRAN_SYM_3; 1.
 DR Neurotransmitter transport; Transmembrane; Glycoprotein;
 KW Symport.
 KM
 FT DOMAIN 1 68
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 FT CARBOHYD 188 188
 FT CARBOHYD 205 205
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 FT CONFLICT 345 345
 FT CONFLICT 354 354
 FT CONFLICT 367 367
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 QY 17 LQATGKRSRVVSLTPARORETAKKAPELLAVGFAVDGNVRFYTCYONGGAF 76
 DB 42 LTSSTLTNPQ--SPVEADRETWGKKIDFLSTVIGFVADLANWRFPLCYKNGGAF 98
 QY 77 LIPYCVMLFEGCLPLFFELALGOVHRCGLTLMKRKICPALKGVAICMIDYMGMYN 136
 DB 99 LVPYLLFMVYIAGMPLFFYMLALGQFNREGAGVWK-ICILVAGVGTVLLISLYOFFIN 157
 QY 137 TIIGAAVYVLIASLASINSVLPWTSQDNEMNPLCTPVTSPQTNPNSS-----TPAK 188
 DB 158 VTIAMALHYL---FSSFTTELPWICNNSMNSPNCSDAHPGDSGSDSLNDTFGTTPAA 214
 QY 189 EFERVNVLEQHSNGLDNGPLKPSALCFVGVFVLYVTSLMKGVRSAGKVVWYATLAY 248
 DB 215 EYFERGVHLHQSHGDDIGPPRMOJTAFLVIVLYLVSMLKGVTSKSVWVIAVWATMY 274
 QY 249 VVLLITLARGVTEPGATEGIRYLLPPEWHKLNQSKWIDAASOIFESLGPFGCTLLATSS 308
 DB 275 VVLTALLRGVTLPGAIDIRAYLSVDFRLCEASWIDAATOVCFSLGCGVLTAPSS 334
 QY 309 YKFNNNCYDALITSSINCLTSFLAGVIFSVLGVMAHVHONKSIEEVLGEGPLGVETVY 368
 DB 335 YKFTNNCYRAIVTTSINSLSFSFGVVFSLGVMQAKHSVPLGVADKADGCLIFITY 394
 QY 369 PEAITMTGCVWVAITFFMLTLTGLDSTFGGLEAVATTAICDEYPRVJGRHREVEYAVLL 428
 DB 395 PEAITPLPSSAMAVVFFIMLTLLTGIDSAMGMESVITGLIDEF-QLLHRRRELFETLL 453

OY 547 IPLYIYKLLIPGNCINRIKTIORPE 573
 DB 571 VPIVATYKFCSLPGSFREKLAIVATPE 597

RESULT 14
 56A3_MOUSE
 ID 56A3_MOUSE STANDARD: PRT: 619 AA.
 AC 061327: 060719: 09R112;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium-dependent dopamine transporter (DA transporter) (DAT).
 GN SLC6A3 OR DAT1 OR DAT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=99307154; PubMed=10373632;
 RA Wu X., Gu H.H.;
 RT "Molecular cloning of the mouse dopamine transporter and
 RL pharmacological comparison with the human homologue.";
 RL Gene 233:163-170(1999).
 RN [2]
 RP SEQUENCE OF 1-343 FROM N.A.
 RC STRAIN=BAB/c; TISSUE=Brain;
 RX MEDLINE=95364623; PubMed=7637582;
 RA Donovan D.M., Vandenberg D.J., Perry M.P., Bird G.S., Ingersoll R.,
 RA Nanthakumar E., Uhl G.R.;
 RT "Human and mouse dopamine transporter genes: conservation of
 RT 5'-flanking sequence elements and gene structures.";
 RL Brain Res. Mol. Brain Res. 30:327-335(1995).
 CC -1- FUNCTION: TERMINATES THE ACTION OF DOPAMINE BY ITS HIGH
 CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
 CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
 CC FAMILY (SNF).
 CC -----
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CC EMBL: AF109072; AAD19643.1;
 CC EMBL: U15791; AA86462.1;
 CC EMBL: U12313; AA86462.1; JOINED.
 CC EMBL: U16265; AAC52283.1;
 CC MGI: MGI:94862; SLC6A3.
 CC InterPro: IPR001175; Na/ntran_symport.
 CC Pfam: PF00209; SNF.1.
 CC PRINTS: PR00176; NANEUSMPORT.
 CC PRODOM: PD000448; Na/ntran_symport.1.
 CC PROSITE: PS00610; NA_NEUOTRAN_SYM_1; 1.
 CC PROSITE: PS00754; NA_NEUOTRAN_SYM_2; 1.
 CC PROSITE: PS0267; NA_NEUOTRAN_SYM_3; 1.
 CC Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
 CC Symport.
 CC DOMAIN 1 68 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 69 89 1 (POTENTIAL).
 CC TRANSMEM 96 116 2 (POTENTIAL).
 CC TRANSMEM 140 160 3 (POTENTIAL).
 CC DOMAIN 161 236 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 237 255 4 (POTENTIAL).
 CC TRANSMEM 264 281 5 (POTENTIAL).
 CC [1]

FT TRANSMEM 317 334 6 (POTENTIAL).
 FT TRANSMEM 346 367 7 (POTENTIAL).
 FT TRANSMEM 400 419 8 (POTENTIAL).
 FT TRANSMEM 446 464 9 (POTENTIAL).
 FT TRANSMEM 480 500 10 (POTENTIAL).
 FT TRANSMEM 521 540 11 (POTENTIAL).
 FT TRANSMEM 559 577 12 (POTENTIAL).
 FT DOMAIN 578 619 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 204 204 N-LINKED (GLCNAc. . .) (POTENTIAL).
 SQ SEQUENCE 619 AA: 68805 MW: 7436137BCB461E9B CRC64;

Query Match 49.0%; Score 1538; DB 1; Length 619;
 Best Local Similarity 49.4%; Pred. No. 1,2e-93;
 Matches 280; Conservative 104; Mismatches 157; Indels 26; Gaps 5;

OY 14 PPDLPATTAOKRSRVASILTPARORETWAKAEFLAVAGFVADLGNVRRPYICONGG 73
 DB 50 PQQT-----VEQEREWTSKIDFLSLVIGFVADLANWRRPYLCYKNG 95

OY 74 GAFLLPYCVMLLEGGPLFFLELALGOYHRCGLTLMKRICPALKGVAICMIDIYGM 133
 DB 96 GAFLLPYLLFVFIAGMPLEFYMELALGQFNREGAGVMK-ICPVLKGVGFYLLISFYVG 154

OY 134 YNTTIIAGVAYVLLASLINSVLPWTSCDNEMNPLCTPYSPTOTNN-----SSTP 186
 DB 155 FYNVIIAVALHYF--FSSFTWDLPIHICNNWNPNCSDAHSSSDGLGINDTFGTTP 211

OY 187 AKFEFFERNVLEOHKNSGLDMGPIKPSIALCFGVFVLYVSLMKGVRSACKVWVWVATA 246
 DB 212 AAEEFERGVYLNHQRGIDDLGPRWQTLACVLIVLYLTSIMKGVATSKVWVWVATM 271

OY 247 PYVULLILLAGVTLPGATEGIRYLTPEWMKLNQSKWIDAASOTIFSLGPGCTLLAL 306
 DB 272 PYVULLILLAGVTLPGATEGIRYLTPEWMKLNQSKWIDAASOTIFSLGPGCTLLAL 331

OY 307 SSYKNFNCRDALITSSINCLTFLAGFYFVSFGMAVHONKSIEVGLGGLVETI 366
 DB 332 SSYKNFTNCRDAITITTSINSLSFSSGFVYFSLGIMACKHNVPIDVATDGLLFTI 391

OY 367 VYPEAIATMTGSVFNAIFFLMLITLGLDSTFGGLEAVTALCODEPYVYLGRHREFAV 426
 DB 392 IYPEAIATLPLISSAAVAFFLLTLGLDLSAMGMSVITGLVDF-QLLRHRELFTLG 450

OY 427 LLLFYIALPPTTYGAYLVLDLNVGPGALILFVFAEAGVWVYGVDRFSEDVATM 486
 DB 451 IYLAFFLLSLFCVYNGGIVYFTLLDHPAAGSILFGLVLEAIGVAMFYGVQOFSDDIKQM 510

OY 487 LGHTGWMFRMCMSYISPVFLVLFVFSVLHHEMLGEGYVPSISIVGWMMTCTVYSC 546
 DB 511 TGQRNLYWRCKMKLVSPCFLLIYVVSIVFRPHYGAIFYPDMANALGMIATSSNAM 570

OY 547 IPLYIYKLLIPGNCINRIKTIORPE 573
 DB 571 VPIVATYKFCSLPGSFREKLAIVATPE 597

RESULT 15
 NTDO_CAEEL
 ID NTDO_CAEEL STANDARD: PRT: 615 AA.
 AC 003614: 09XTR0;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium-dependent dopamine transporter (DA transporter) (DAT).
 GN T2365.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Felodertinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-98440631; PubMed-9765501;
 RA Jayanthi L.D., Apparundaram S., Malone M.D., Ward E., Miller D.M.,
 RA Eppler M., Blakely R.D.;
 RT "The Caenorhabditis elegans gene T3G5.5 encodes an antidepressant and
 RT cocaine-sensitive dopamine transporter.";
 RN Mol. Pharmacol. 54:601-609(1998).
 RN (2)
 RN SEQUENCE FROM N.A.
 RP STRAIN-Bristol N2;
 RX MEDLINE-94150718; PubMed-7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Wainstock L., Wilkinson-Sproat J.,
 RA Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RN Nature 368:32-38(1994).
 RN (3)
 RN REVISIONS.
 RA Durbin R.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TERMINATES THE ACTION OF DOPAMINE BY ITS HIGH
 CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
 CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
 CC -1- SIMILARITY: BELONGS TO THE SODIUM-NEUROTRANSMITTER SYMPORTER
 CC FAMILY (SNF).
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 CC -----
 DR EMBL: AF079899; AAC83661.1; -
 DR EMBL: Z19158; CAAT9575.2; -
 DR EMBL: Z19156; CAAT9575.2; JOINED.
 DR EMBL: Z19156; CAAT9564.2; -
 DR EMBL: Z19158; CAAT9564.2; JOINED.
 DR PIR: S28306; S28306.
 DR WormPep: T23G5.5; CE25124.
 DR InterPro: IPR000175; Na/nttran_symport.
 DR Pfam: PR00209; SNF.1
 DR PRINTS: PR00176; NANEUSMPORT.
 DR ProDom: PD000448; Na/nttran_symport; 2.
 DR PROSITE: PS00610; NA_NEUROTRAN_SYM_1; 1.
 DR PROSITE: PS00754; NA_NEUROTRAN_SYM_2; 1.
 DR PROSITE: PS0267; NA_NEUROTRAN_SYM_3; 1.
 DR Neurotransmitter transport; Transmembrane; Glycoprotein;
 KM Symport.
 FT DOMAIN 1 48
 FT TRANSMEM 49 69 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 94 1 (POTENTIAL).
 FT TRANSMEM 125 145 2 (POTENTIAL).
 FT TRANSMEM 146 232 3 (POTENTIAL).
 FT TRANSMEM 233 253 4 (POTENTIAL).
 FT TRANSMEM 258 278 5 (POTENTIAL).
 FT TRANSMEM 344 364 6 (POTENTIAL).
 FT TRANSMEM 371 391 7 (POTENTIAL).
 FT TRANSMEM 393 413 8 (POTENTIAL).
 FT TRANSMEM 440 460 9 (POTENTIAL).
 FT TRANSMEM 462 482 10 (POTENTIAL).

FT TRANSMEM 515 535 11 (POTENTIAL).
 FT TRANSMEM 550 570 12 (POTENTIAL).
 FT DOMAIN 571 615 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 162 162 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 615 AA: 69265 MW: 69265 MW: ODA2876EB3AC8049 CRC64;
 Query Match 45.0%; Score 1412; DB 1; Length 615;
 Best Local Similarity 46.3%; Pred. No. 2, 1e-85;
 Matches 276; Conservative 103; Mismatches 177; Indels 40; Gaps 9;
 QY 14 PPDLPATTAQKSRVSVSLTPARQRETMWAKAEFLAVGVAVDGLGNWRFYICQNGG 73
 DB 26 PIGDPVNTPEKX-----PA---RQWSGKIDFLSVGVFAVDLGNMRFPLCKNGG 75
 QY 74 GALLIYCVWLLFGGLPLFLEALQYHRCGLTLTKRCPLKQVGAICIDIDYMGK 133
 DB 76 GVPLIYSLIWLTLTGGLPLFYMELCLQYRKGAITTWGRICPLKIGICVILTAFYDF 135
 QY 134 YNTIIGMAVYLLASIASINSVLPWTCSDNENPTLC-----TPVTSPTNPSS--- 184
 DB 136 FTVVILLAMGLHYITSF-SFN--LPWASCNNSINSPACYPHNSDGTAMCRSANSVSA 192
 QY 185 ---TPAKFEERNVLEQHSN-----GLDDMGPIKBSLALCVGEVLYVYSLMKV 233
 DB 193 EKISAEEYFKGLCLHEANAPNSHVIRSVTDLGAVRMIDALSLFVYLICYSWMKG 252
 QY 234 RSAGKYVWYVY 293
 DB 253 HTSGKVVWYVY 312
 QY 294 FSLGPGFTLLALSYNKNFNNCYRDLITSSINCLTSLFAGVIFSVLGYMAHYONKSI 353
 DB 313 FSLGPGFTLLALSYNKNFNNCYRDLITSSINCLTSLFAGVIFSVLGYMAHYONKSI 372
 QY 354 EYVGLGPGFTLLALSYNKNFNNCYRDLITSSINCLTSLFAGVIFSVLGYMAHYONKSI 413
 DB 373 EAVAOEGPGVLFVY 432
 QY 414 RVIGRRREVFVY 473
 DB 433 -ILKNREVFVY 491
 QY 474 YGVDRFSEDEVRTMLGHTPGFMFRTCSYISPVFLVLFVSVLAHEMLGGEYTPSWSI 533
 DB 492 YGLRGFVHDVYKEMGRPGNWKFCWSCAPRLLISMIISNFINYQALTYQDITTYTAA 551
 QY 534 YVGVWMTGTTVSCIPLYIYKLLITPGNCINR-----IKTQREPVTSIPADST 583
 DB 552 VIGIIFALSGASFIPLVGYIKFVNARGNTISEKMWQRTMRYRKRPNQTEYIPIPT 607
 Search completed: July 18, 2003, 21:59:24
 Job time : 23 secs

